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Traitmill™: a functional genomics platform for the phenotypic analysis of cereals

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Abstract

The improvement of quality and quantitative traits in industrial crops is among the most important goals in plant breeding. Many traits of interest are controlled by multiple genes and improvements have so far only been obtained through conventional breeding. The use of biotechnological tools to modify quantitative traits is highly challenging. CropDesign has developed TraitMill™, an automated plant evaluation platform allowing high-throughput testing of the effect of plant-based transgenes on agronomically valuable traits in crop plants. The focus of the platform is currently on rice, a good model for other important cereals such as maize and wheat. TraitMill™ offers a high-throughput prediction of gene function. Genes of validated function that confer trait improvement can then be transferred to other cereal crop species such as maize, but also to dicots, trees and ornamentals. TraitMill™ involves the following key components: (i) selection of candidate trait improvement genes among genes involved in signal transduction, cell cycle control, transcription, nutrient metabolism, etc.; (ii) a suite of validated constitutive or tissue-specific promoters from rice allowing for the selection of the most appropriate promoter–gene combination in view of the desired trait improvement; (iii) an industrialized plant transformation system generating tens of thousands of transgenic plants annually; and (iv) a robotized trait evaluation set-up for plant evaluation, proprietary image analysis software for measuring plant performance parameters and statistical analysis of results.

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References

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GT Beemster , V Mironov and D lnze (2005) Tuning the cell-cycle engine for improved plant performance. *Current Opinions in Biotechnology* 16: 142–146.

L De Veylder , T Beeckman , GT Beemster , L Krols , F Terras , I Landrieu , E van der Schueren , S Maes , M Naudts and D Inze (2001) Functional analysis of cyclin-dependent kinase inhibitors of Arabidopsis. *Plant Cell* 13: 1653–1668.

L De Veylder , T Beeckman , GT de Beemster , J Almeida Engler , S Ormenese , S Maes , M Naudts , E Van Der Schueren , A Jacqmard , G Engler and D Inze (2002) Control of proliferation, endoreduplication and differentiation by the Arabidopsis E2Fa-DPa transcription factor. *EMBO Journal* 21: 1360–1368.

W Van Camp (2005) Yield enhancement genes: seeds for growth. *Current Opinions in Biotechnology* 16: 147–153.

K Vandepoele , J Raes , L De Veylder , P Rouze , S Rombauts and D Inze (2002) Genome-wide analysis of core cell cycle genes in Arabidopsis. *Plant Cell* 14: 903–916.

H Wang , Y Zhou , S Gilmer , S Whitwill and LC Fowke (2000) Expression of the plant cyclin-dependent kinase inhibitor ICK1 affects cell division, plant growth and morphology. *Plant Journal* 24: 613–623.